



## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/306,780

DATE: 04/23/2002

TIME: 11:00:00

Input Set : N:\Crf3\RULE60\09306780.raw

Output Set: N:\CRF3\04232002\I306780.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: TAKEMURA, FUMINORI

6 UENO, EIICHI

7 ITOH, SATORU

9 (ii) TITLE OF INVENTION: NUCLEIC ACID-BOUND POLYPEPTIDE, METHOD  
 10 OF PRODUCING NUCLEIC ACID-BOUND POLYPEPTIDE AND  
 11 IMMUNOASSAY USING THE POLYPEPTIDE.

13 (iii) NUMBER OF SEQUENCES: 20

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,  
 17 P.C.

18 (B) STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

19 (C) CITY: ARLINGTON

20 (D) STATE: VA

21 (E) COUNTRY: U.S.A.

22 (F) ZIP: 22202

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk

26 (B) COMPUTER: IBM PC compatible

27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

30 (vi) CURRENT APPLICATION DATA:

C--&gt; 31 (A) APPLICATION NUMBER: US/09/306,780

C--&gt; 32 (B) FILING DATE: 07-May-1999

33 (C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: US/08/841,657A

38 (B) FILING DATE: 30-APR-1997

40 (A) APPLICATION NUMBER: JP 8-134444

41 (B) FILING DATE: 01-MAY-1997

43 (viii) ATTORNEY/AGENT INFORMATION:

44 (A) NAME: OBLON, NORMAN F.

45 (B) REGISTRATION NUMBER: 24,618

46 (C) REFERENCE/DOCKET NUMBER: 2084-033-0

48 (ix) TELECOMMUNICATION INFORMATION:

49 (A) TELEPHONE: (703) 413-3000

50 (B) TELEFAX: (703) 413-2220

53 (2) INFORMATION FOR SEQ ID NO: 1:

55 (i) SEQUENCE CHARACTERISTICS:

56 (A) LENGTH: 102 base pairs

57 (B) TYPE: nucleic acid

58 (C) STRANDEDNESS: single

ENTERED

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59      (D) TOPOLOGY: linear
61      (ii) MOLECULE TYPE: other nucleic acid
62      (A) DESCRIPTION: /desc = "synthetic DNA"
65      (ix) FEATURE:
66          (A) NAME/KEY: CDS
67          (B) LOCATION: 1..102
70      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
72 AGA CGA CGA GGG AGG TCC CCT AGA AGA AGA ACT CCC TCG CCT CGC AGA      48
73 Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro Arg Arg
74  1          5          10          15
76 CGA AGG TCT AAA TCG CCG CGT CGC AGA AGA TCT CAA TCT CGG GAA TCT      96
77 Arg Arg Ser Lys Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg Glu Ser
78          20          25          30
80 CAA TGT      102
81 Gln Cys
85 (2) INFORMATION FOR SEQ ID NO: 2:
87      (i) SEQUENCE CHARACTERISTICS:
88          (A) LENGTH: 34 amino acids
89          (B) TYPE: amino acid
90          (D) TOPOLOGY: linear
92      (ii) MOLECULE TYPE: protein
94      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
96 Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro Arg Arg
97  1          5          10          15
99 Arg Arg Ser Lys Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg Glu Ser
100          20          25          30
102 Gln Cys
105 (2) INFORMATION FOR SEQ ID NO: 3:
107      (i) SEQUENCE CHARACTERISTICS:
108          (A) LENGTH: 360 base pairs
109          (B) TYPE: nucleic acid
110          (C) STRANDEDNESS: single
111          (D) TOPOLOGY: linear
113      (ii) MOLECULE TYPE: other nucleic acid
114          (A) DESCRIPTION: /desc = "synthetic DNA"
117      (ix) FEATURE:
118          (A) NAME/KEY: CDS
119          (B) LOCATION: 1..360
122      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
124 ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC      48
125 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
126  1          5          10          15
128 CGC CGC CCA CAG GAC GTT AAG TTC CCG GGC GGT GGT CAG ATC GTT GGT      96
129 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
130          20          25          30
132 GGA GTT TAC CTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG      144
133 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
134          35          40          45
136 ACT AGG AAG ACT TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT      192

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137 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
138      50                      55                      60
140 ATC CCC AAG GCT CGC CGG CCC GAG GGT AGG ACC TGG GCT CAG CCC GGG      240
141 Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly
142 65                      70                      75                      80
144 TAC CCT TGG CCC CTC TAT GGC AAC GAG GGT ATG GGG TGG GCA GGA TGG      288
145 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp
146                      85                      90                      95
148 CTC CTG TCA CCC CGT GGC TCT CGG CCT AGT TGG GGC CCC ACA GAC CCC      336
149 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
150      100                      105                      110
152 CGG CGT AGG TCG CGT AAT TTG GGT      360
153 Arg Arg Arg Ser Arg Asn Leu Gly
154      115                      120
157 (2) INFORMATION FOR SEQ ID NO: 4:
159     (i) SEQUENCE CHARACTERISTICS:
160         (A) LENGTH: 120 amino acids
161         (B) TYPE: amino acid
162         (D) TOPOLOGY: linear
164     (ii) MOLECULE TYPE: protein
166     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
168 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
169 1      5      10      15
171 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
172      20      25      30
174 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
175      35      40      45
177 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
178      50      55      60
180 Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly
181 65      70      75      80
183 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp
184      85      90      95
186 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
187      100      105      110
189 Arg Arg Arg Ser Arg Asn Leu Gly
190      115      120
192 (2) INFORMATION FOR SEQ ID NO: 5:
194     (i) SEQUENCE CHARACTERISTICS:
195         (A) LENGTH: 450 base pairs
196         (B) TYPE: nucleic acid
197         (C) STRANDEDNESS: single
198         (D) TOPOLOGY: linear
200     (ii) MOLECULE TYPE: other nucleic acid
201         (A) DESCRIPTION: /desc = "synthetic DNA"
204     (ix) FEATURE:
205         (A) NAME/KEY: CDS
206         (B) LOCATION: 1..450
209     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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211	ATG	AGC	ACA	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	AAC	ACC	AAC	48
212	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn	
213	1				5					10						15	
215	CGC	CGC	CCA	CGG	GAC	GTT	AAA	TTC	CCG	GGC	GGT	GGT	CAG	ATC	GTT	GGT	96
216	Arg	Arg	Pro	Arg	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly	
217				20					25					30			
219	GGA	GTT	TAC	CTG	TTG	CCG	CGC	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	144
220	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala	
221			35					40					45				
223	ACT	AGG	AAG	ACT	TCC	GAG	CGG	TCG	CAA	CCT	CGT	GGA	AGG	CGA	CAA	CCT	192
224	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	
225		50					55					60					
227	ATC	CCC	AAG	GCT	CGC	CGG	CCC	GAG	GGT	AGG	ACC	TGG	GCT	CAG	CCC	GGG	240
228	Ile	Pro	Lys	Ala	Arg	Arg	Pro	Glu	Gly	Arg	Thr	Trp	Ala	Gln	Pro	Gly	
229	65					70				75					80		
231	TAC	CCT	TGG	CCC	CTC	TAT	GGC	AAC	GAG	GGT	ATG	GGG	TGG	GCA	GGA	TGG	288
232	Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Met	Gly	Trp	Ala	Gly	Trp	
233				85					90					95			
235	CTC	CTG	TCA	CCC	CGT	GGC	TCC	CGG	CCT	AGT	TGG	GGC	CCC	ACG	GAC	CCC	336
236	Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Thr	Asp	Pro	
237			100						105					110			
239	CGG	CGT	AGG	TCA	CGC	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACA	TGC	384
240	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	
241			115					120					125				
243	GGC	TTC	GCC	GAC	CTC	ATG	GGG	TAC	ATT	CCG	CTT	GTC	GGC	GCC	CCC	CTA	432
244	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	
245		130				135						140					
247	GGG	GGC	GCT	GCC	AGG	GCC											450
248	Gly	Gly	Ala	Ala	Arg	Ala											
249	145					150											
252	(2)	INFORMATION FOR SEQ ID NO: 6:															
254		(i) SEQUENCE CHARACTERISTICS:															
255		(A) LENGTH: 150 amino acids															
256		(B) TYPE: amino acid															
257		(D) TOPOLOGY: linear															
259		(ii) MOLECULE TYPE: protein															
261		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:															
263	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn	
264	1				5					10					15		
266	Arg	Arg	Pro	Arg	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly	
267				20					25					30			
269	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala	
270			35					40					45				
272	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	
273		50					55					60					
275	Ile	Pro	Lys	Ala	Arg	Arg	Pro	Glu	Gly	Arg	Thr	Trp	Ala	Gln	Pro	Gly	
276	65					70				75					80		
278	Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Met	Gly	Trp	Ala	Gly	Trp	
279				85					90					95			

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```

281 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
282      100      105      110
284 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
285      115      120      125
287 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu
288      130      135      140
290 Gly Gly Ala Ala Arg Ala
291 145      150
293 (2) INFORMATION FOR SEQ ID NO: 7:
295     (i) SEQUENCE CHARACTERISTICS:
296         (A) LENGTH: 483 base pairs
297         (B) TYPE: nucleic acid
298         (C) STRANDEDNESS: single
299         (D) TOPOLOGY: linear
301     (ii) MOLECULE TYPE: other nucleic acid
302         (A) DESCRIPTION: /desc = "synthetic DNA"
305     (ix) FEATURE:
306         (A) NAME/KEY: CDS
307         (B) LOCATION: 1..483
310     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
312 ATG GCT AGC GAA TTC ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC      48
313 Met Ala Ser Glu Phe Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr
314 1      5      10      15
316 AAA CGT AAC ACC AAC CGC CGC CCA CAG GAC GTT AAG TTC CCG GGC GGT      96
317 Lys Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly
318      20      25      30
320 GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC AGG GGC CCC AGG      144
321 Gly Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg
322      35      40      45
324 TTG GGT GTG CGC GCG ACT AGG AAG ACT TCC GAG CGG TCG CAA CCT CGT      192
325 Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg
326      50      55      60
328 GGA AGG CGA CAA CCT ATC CCC AAG GCT CGC CGG CCC GAG GGT AGG ACC      240
329 Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr
330 65      70      75      80
332 TGG GCT CAG CCC GGG TAC CCT TGG CCC CTC TAT GGC AAC GAG GGT ATG      288
333 Trp Ala Gln Pro Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met
334      85      90      95
336 GGG TGG GCA GGA TGG CTC CTG TCA CCC CGT GGC TCT CGG CCT AGT TGG      336
337 Gly Trp Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp
338      100      105      110
340 GGC CCC ACA GAC CCC CGG CGT AGG TCG CGT AAT TTG GGT GGA TCC AGA      384
341 Gly Pro Thr Asp Pro Arg Arg Arg Ser Arg Asn Leu Gly Gly Ser Arg
342      115      120      125
344 CGA CGA GGC AGG TCC CCT AGA AGA AGA ACT CCC TCG CCT CGC AGA CGA      432
345 Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro Arg Arg Arg
346      130      135      140
348 AGG TCT AAA TCG CCG CGT CGC AGA AGA TCT CAA TCT CGG GAA TCT CAA      480
349 Arg Ser Lys Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg Glu Ser Gln

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VERIFICATION SUMMARY

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L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]